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July 28, 2000

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ATTORNEY DOCKET NO. 03495-0193

Box PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Re: New U.S. Patent Application
Title: Detection of a Gene, *vatD*, Encoding an
Acetyltransferase Inactivating Streptogamin
Inventor(s): J. Haroche et al.

Sir:

We enclose the following papers for filing in the United States Patent and Trademark Office in connection with the above patent application.

1. Application - 48 pages, including 6 independent claim(s) and 41 claims total.
2. Drawings - 3 sheets of informal drawings (Figures 1-3).
3. Preliminary Amendment.
4. Request for Approval of Drawing Change.
5. A check for \$1,562.00 representing a \$690.00 filing fee and \$872.00 for additional claims fees.

Applicants claim the right to priority based on Provisional Patent Application No. 60/146,141 filed July 30, 1999.

This application is being filed under the provisions of 37 C.F.R. § 1.53(f).
Applicant(s) await notification from the Patent and Trademark Office of the time set for filing the Declaration.

FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P.

Assistant Commissioner for Patents

July 28, 2000

Page 2

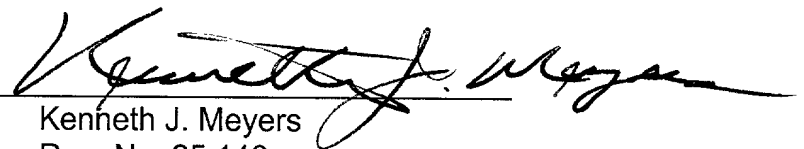
Please accord this application a serial number and filing date.

The Commissioner is hereby authorized to charge any additional filing fees due and any other fees due under 37 C.F.R. § 1.16 or § 1.17 during the pendency of this application to our Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

By:



Kenneth J. Meyers
Reg. No. 25,146

KJM/SMP:
Enclosures

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)	
)	
Julien HAROCHE et al.)	
)	
Serial No.: Not Yet Assigned)	Group Art Unit: Not Yet Assigned
)	
Filed: Concurrently herewith)	Examiner: Not Yet Assigned
)	
For: DETECTION OF A GENE, <i>vatD</i> ,)	
ENCODING AN ACETYLTRANSFERASE)	
INACTIVATING STREPTOGRAMIN)	

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

PRELIMINARY AMENDMENT

Prior to examination of the above-identified application, please amend the application as follows.

IN THE DRAWINGS:

Please amend Figures 1 and 2 as indicated in the attached Request for Approval of Drawing Changes.

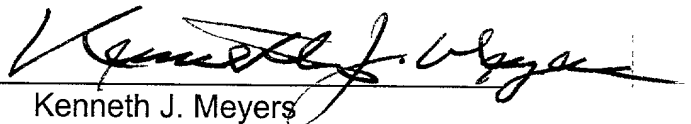
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If there is any fee due in connection with the filing of this Preliminary
Amendment, please charge the fee to our Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
GARRETT & DUNNER, L.L.P.

By: 
Kenneth J. Meyers
Reg. No. 25,146

Date: July 28, 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)	
)	
Julien HAROCHE et al.)	
)	
Serial No.: Not Yet Assigned)	Group Art Unit: Not Yet Assigned
)	
Filed: Concurrently herewith)	Examiner: Not Yet Assigned
)	
For: DETECTION OF A GENE, <i>vatD</i> ,)	
ENCODING AN ACETYLTRANSFERASE)		
INACTIVATING STREPTOGRAMIN)		

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

REQUEST FOR APPROVAL OF DRAWING CHANGE

Subject to the approval of the Examiner, it is respectfully requested that Figures 1 and 2 in the above-captioned application be amended by insertion of sequence identifiers SEQ ID NO:17 and SEQ ID NO:18 (Figure 1) and SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:18 (Figure 2) in the upper left-hand corners of the figures. The changes are indicated in red on the attached copy of the originally filed drawings.


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PATENT
Attorney Docket No. 3495.0193

Upon approval of the proposed changes, Applicants respectfully request that the submission of revised drawings be deferred until after a notice of allowance has issued.

Respectfully submitted,
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Kenneth J. Meyers
Reg. No. 25,146

Date: July 27, 2000

SEQ ID NO. 17

1 CCCTTTAAAG AGGGCTTTTA TATATTAATC ACAAATCACT TATCACAAAT
 51 CACAAGTGAT TTGTGATTGT TGATGATAAA ATAAGAATAA GAAGAAATAG
 101 AAAGAAGTGA GTGATTGTGG GAAATTTAGG CGCACAAAAA GAAAGAGTGT
 151 GACAAAACAT GGTTATGCTA CATGTTTAAG GTAAAAATAG TTATGTCACA
 201 ACTACTTATT TTTTACCCTA ATCTTCTAGA CTATAATTAA AATTAAATAA

XbaI

251 CTCAATTCGG AGGTACTAAC ATGACTATAC CTGACGCAA TGCAATCTAT

SEQ ID NO 18

RBS

START

H N S A I K E V V F I K N V I K S
 301 CATACTCAG CCATCAAAGA GGTGTCTTT ATCAAGAACG TGATCAAAAG

DdeI

DpnI

P N I E I G D Y T Y Y D D P V N
 351 TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC

SspI

P T D F E K H V T H H Y E F L G D
 401 CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC

K L I I G K F C S L A S G I E F I
 451 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT

M N G A N H V M K G I S T Y P F
 501 CATGAACGGT GCCAACCACG TAATGAAAGG TATTTCTGACT TATCCATTTA

TaqI

N I L G G D W Q Q Y T P E L T D L
 551 ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAAC TACTGATTTG

P L K G T V V G N D V W F G Q N V
 601 CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA

T V L P G V K I G D G A I I G A
 651 TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG

N S V V T K D V A P Y T I V G G N
 701 CAAATAGTGT TGTAACAAA GACGTCGCTC CATATACAAT TGTCGGTGGC

P I Q L I G P R F E P E V I Q A L
 751 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGAAG TTATTCAAGC

XmnI

E N L A W W N K D I E W I T A N
 801 ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG ATAAGTCTA

N V P K L M Q T T P T L E L I N S
 851 ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT

L M E K *

STOP

901 TTAATGGAAA AATAAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT
 951 TGTTTACACG GCTTTTACTA TTTAGTGAAT CCAATTTATT AATAATAGAT

HaeIII

1001 ATGATATACC AGTAAAAAAT AACTAGCCA CCTCTGGCGG TACTCTACTC
 1051 GTATATTTTA TTTACGACCT TCTGATGATA

FIGURE 1

Vat
VatC
SatA
VatB
VatD

Vat
VatC
SatA
VatB
VatD

Vat
VatC
SatA
VatB
VatD

LNLNNDHGPDPENILPIKGNRLQFIKPTITN-ENILVGEYSYDSDKRG-ESFEDQVLTH
MKWQOQGNPEEIYPIEGNKHVQFIKPSITK-PNILVGEYSYDSDKG-ESFESQVLTH
-----MGPNPMKMPPIEGNKSVOFIKPILEKLENVEVEYSYDSDKG-ETFDKQILYH
-----MKYGPDPNSIYPHEEIKSVCFIKNTITN-PNIVGDYTYXSDVNGAEKEFEHVTHH
-----MTLPDANAIIYHNSAIKEVFIKNVICS-PNIEIGDYTYXDDPVNPTDFEKHVTHH
.:
YEVI GDKL IIGRFCSIGPGTTFIMGANHRMDG-STYPFHLFRMGWEKMPSLKDLPLKG
YELIGDKLILGKFCSIGPGTTFIMGANHRMDG-STFPNLFNGWEKHTPTLEDLPLKG
YPLNDKLKIGKFCSIGPGVTIIMGANHRMDG-STYPNLFNGWEKHPKLDQPLIKG
YFPRGDKLVIGKFCALAEIEFIMGANHRMNSTITYPFNIMGNGWEKATPSLEDLPLFG
YFELGDKLIGKFCSLASGIEFIMGANHV MKGI STYPFNILGWDWQYTPPELTDLPLKG
.:
DIEIGNDVWIGRDVTIMPVGKIGDGAIIAAEAVVTKNVAPYSIVGNGNPLKFIKKRFSGDV
NTEIGNDVWIGRDVTIMPVGKIGNGAIIAAKSVTTKNVDPYSVVGNGNPSRLIKIRFSKEK
DTIIGNDVWIGKDVIMPVGKIGDGAIVAANSVVKDIAPYMLAGNPANEIKORFDQDT
DTVVGNDVWIGQNVITMFGIQIGDGAIVAANSVVTKDVPYRIIGGNPSRIKKRFEDEL
DTVVGNDVWFGQNVITVLPVGKIGDGAIIIGANSVVTKDVAPTYIVGNGNPIQLIGPRFEPEV
.:*
IEEWLALQWNNLDMKIINENLPIING--DIEMLKRRKLLDDT
IAALLKVRWWDLEIETINENIDCILG--DIKKVKRS-----
INQLLDIKWNNPIDIINENIDKILDN--SIIREVWK-----
IDYLLQIKWWDWSAQIFSNLETLCS--DLEKIKSIRD-----
IQALENLAWWNKDIEWITANVPKLMQTPTPELINSIMEK-----
.:.

FIGURE 2

Atty. Docket No: 03495.0193

UNITED STATES PATENT APPLICATION

OF

JULIEN HAROCHE

JEANINE ALLIGNET

AND

NEVINE EL SOLH

FOR

DETECTION OF A GENE, *vatD*, ENCODING AN
ACETYLTRANSFERASE INACTIVATING STREPTOGRAMIN

BACKGROUND OF THE INVENTION

This application claims the right to priority based on Provisional Patent Application No. 60/146,141 filed July 30, 1999. The entire disclosure of Provisional Patent Application No. 60/146,141 is hereby incorporated by reference.

This invention relates to the discovery of a new gene, *vatD*, encoding an acetyltransferase inactivating streptogramin A, which is widely distributed in virginiamycin-resistant *enterococcus faecium* strains.

Streptogramin, virginiamycin, pristinamycin, and synergistin are produced by streptomyces, and consist of synergistic mixtures of two chemically different molecules: A and B compounds (10). In some European countries and in Algeria, these mixtures are used both orally and topically, mostly against staphylococcal infections. Virginiamycin is used as growth promoter in animal feed in Europe and in the U.S.A. Virginiamycin-resistant *Enterococcus faecium* are prevalent in fecal and intestinal samples from turkeys, pigs, broilers, and farmers in Europe and America (1, 14, 19, 20). Since bacteria can be transferred via food from animals to humans, this is alarming, in particular because quinupristin/dalfopristin (J. Antimicrob. Agents Chemother., 1992, 30[suppl.30]), an injectable mixture of semi-synthetic streptogramins soon to be commercialized (Synercid), is expected to be widely used, mainly to treat vancomycin-resistant *E. faecium* infections.

The *satA* gene (18) encoding an acetyltransferase inactivating A compounds was isolated from an *E. faecium*

5 plasmid. It was found in only 29 % of the 140 tested
E. faecium strains isolated in Dutch and Danish farms and
resistant to the mixtures (13, 14). Five of the *E.*
faecium strains isolated in Denmark harbored a large
10 plasmid conferring resistance to the mixture and which
was transferable by filter mating experiments to an *E.*
faecium recipient (14). None of the transconjugants
harboring these plasmids carried *satA*, *vat*, *vatB*, *vga*, or
vgaB (14). These results suggested that the *E. faecium*
strains contained other unidentified streptogramin A
resistance gene(s). Thus, there continues to exist a
need in the art for the identification of new genes
specific for *Enterococcus faecium* resistant to
streptogramin A and related compounds.

15 SUMMARY OF THE INVENTION

Accordingly, this invention aids in fulfilling this
need in the art by providing a new gene, *vatD*, encoding
an acetyltransferase inactivating Streptogramin A, which
is widely distributed in virginiamycin-resistant
20 *Enterococcus faecium* strains. In particular, this
invention provides a purified peptide-comprising the
complete amino acid sequence (SEQ ID NO:1) encoded by the
vatD gene. This invention also provides polypeptide
fragments derived from SEQ ID NO:1 containing at least 10
25 amino acids. The fragments can be common to all
virginiamycin A acetyl transferases as shown on SEQ ID
NOS:5, 6, 7, and 8. The fragments according to the
invention can be specific of as shown on SEQ ID NOS:9,
10, 11, and 12.

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This invention additionally provides a purified polynucleotide comprising the complete nucleic acid sequence of the *vatD* gene (SEQ ID NO:2). This invention also provides nucleic acid fragments derived from SEQ ID NOS:3 and 4 containing 15 to 40 nucleotides as primers F and R. For example, the fragments are those corresponding to nucleotides No. 899 to 878 and to nucleotides No. 354 to nucleotide 378. (Fig. 1)

In addition, two primers have been selected in order to obtain, after using an amplification technique and after cloning the amplified sequence, the complete gene of *vatD* capable of being expressed in *Staphylococcus aureus* (strain No. 4220 described by KREISWIRTH et al. in Nature 1983, Vol. 306, pp. 709-712]. These primers are shown in SEQ ID NOS:13 and 14 as *vatDA* and *vatDB*. The *vatDA* is from nucleotide 98 to nucleotide 120 (Figure 1). The *vatDB* is from nucleotide 982 to nucleotide 957 (Figure 1).

In SEQ ID NOS:13 and 14, an artificial site was created if comparing with the original sequence in Figure 1 at nucleotides No. 107 and 109 where G was replaced by T and G was replaced by C, respectively. An *EcoRI* site was then produced in the first primer. In the same manner, in SEQ ID NOS:3 and 4, at nucleotide No. 362, A replaces G (as in the original sequence) and at nucleotide 367, C replaces G (as in the original sequence). A new *EcoRI* site was created. In the second primer of SEQ ID NOS:3 and 4, a new *EcoRI* site was created by replacing at nucleotide No. 891 G by C and on the complementary strand (as shown) the base C (original) is replaced by G.

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This invention also provides a composition comprising purified polynucleotide sequences including at least one nucleotide sequence of the genes selected from the group consisting of synthetic polynucleotides or fragments of genes or cDNA of *vatD* useful for the detection of resistance to streptogramin A and related compounds. The gene *vatD* was obtained from a *Hind*III fragment of 5 kb prepared from *enterococcus faecium* genome (strain K14) after digestion by *Hind*III restriction enzyme. The *Hind* III fragment hybridizes with an amplicon containing two degenerated or consensus primers referred to as M and N, which are defined as SEQ ID NOS:5, 6, 7, and 8. This amplicon has 147 nucleotides. The amplicon or the two degenerated primers (M and N) can be used for the preparation of DNA chips as taught in PCT applications No. W095.11.995 and No. WO 97.02.357. The sequences upstream and downstream of this amplicon were obtained.

The DNA fragment containing the *vatD* gene including the amplicon is shown in Figure 1. A region having in this said fragment, the possible properties of a bacterial promoter activity is located as follows in Figure 1. Its sequence is:

```

                                     -35
                                     TGTCACA
                                     -10
201  ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAAT
                                     XbaI

```

(SEQ ID NO:16)

Additionally, the invention includes a purified polynucleotide that hybridizes specifically under

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stringent conditions with a polynucleotide of SEQ ID NOS:
2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12.

5 The invention further includes polynucleotide
fragments comprising at least 10 nucleotides capable of
hybridization under stringent conditions with any one of
the nucleotide sequences enumerated above.

10 In another embodiment of the invention, a
recombinant DNA sequence comprising at least one
nucleotide sequence enumerated above and under the
control of regulatory elements that regulate the
expression of resistance to antibiotics of the
streptogramin family in a defined host is provided. The
amplified complete gene of vatD, including the amplicon
and the promoter, is shown in SEQ ID NO:15.

15 Furthermore, the invention includes a recombinant
vector comprising the recombinant DNA sequence noted
above, wherein the vector comprises the plasmid pIP 1801
contained in *E. coli*. The recombinant strain has been
deposited at the collection C.N.C.M. in Paris, France,
20 under the accession number I-2247 on July 7, 1999.

The invention also includes a recombinant cell host
comprising a polynucleotide sequence enumerated above or
the recombinant vector defined above.

25 In still a further embodiment of the invention, a
method detecting bacterial strains that contain the
polynucleotide sequences set forth above is provided.

Additionally, the invention includes kits for the
detection of the presence of bacterial strains that
contain the polynucleotide sequences set forth above.

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The invention also contemplates antibodies recognizing peptide fragments or polypeptides encoded by the polynucleotide sequences enumerated above.

Still further, the invention provides for a screening met for active antibiotics and/or molecules for the treatment of infections due to Gram-positive bacteria, particularly enterococci, based on the detection of activity of these antibiotics and/or molecules on bacteria having the resistance phenotype to streptogramins.

BRIEF DESCRIPTION OF THE DRAWINGS

This invention will be more fully described with reference to the drawings in which:

FIGURE 1 discloses the complete nucleotide and amino acid sequences of *vatD*. In this Figure are also represented the upstream and downstream regions of the *vatD* gene.

FIGURE 2 is a comparison between the sequences of *vatD* protein and four acetyltransferase enzymes already published.

FIGURE 3 is a restriction map of the insert of 1080 bp contained in the plasmid deposited in *E. coli* at C.N.C.M. I-2247.

DETAILED DESCRIPTION OF THE INVENTION

The present invention pertains to polynucleotides derived from *Enterococcus faecium* genes encoding resistance to streptogramin A and chemically related compounds. This invention also relates to the use of the polynucleotides as oligonucleotide primers or probes for

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detecting *Enterococcus faecium* strains that are resistant to streptogramin A and related compounds in a biological sample.

5 In another embodiment, the present invention is directed the full length coding sequences of the *Enterococcus faecium* genes encoding resistance to streptogramin A and to the polypeptides expressed by these full length coding sequences.

10 Further, this invention relates to the use of the expressed polypeptides to produce specific monoclonal or polyclonal antibodies that serve as detection means in order to character any *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A and chemically related compounds

15 The present invention is also directed to diagnostic method for detecting specific strains of *Enterococcus faecium* expected to be contained in a biological sample. The diagnostic methods use the oligonucleotide probes and primers as well as the antibodies of the invention.

20 More particularly, it has now been determined that bacteria from the *Enterococcus faecium* genus carry a *vatD* gene, which confers resistance to streptogramin A. A gene encoding an acetyltransferase inactivating streptogramin A was isolated from an *Enterococcus faecium*
25 strain and sequenced. The gene, designated *vatD*, encodes a 23,775 kDa protein exhibiting 48.5 to 59.9 % amino acid identity with four other enzymes with the same activity,

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vat, vatB, vatC, and satA. The calculation of the percentage of identity was made by using the program gap of GCG software (version 9.1). The parameters are chosen as follows:

- 5 a) for amino acid comparisons:
 gap penalty: 12
 gap extension penalty: 4
 length: the sequence to be compared in SEQ ID
 NO:1 having 213 amino acids.
- 10 b) for nucleotide comparisons:
 gap penalty: 50
 gap extension penalty: 3.

Figure 2 shows the comparative amino acid alignments of vatD with four virginiamycin A acetyl transferase proteins. The satB protein is from *Enterococcus*, and vat, vatB, and vatC are from *Staphylococcus*.

Novel polynucleotides corresponding to the vatD gene from various strains of *Enterococcus faecium* have been isolated and sequenced. These polynucleotides include
20 SEQ ID NO:2. By "polynucleotides" according to the invention is meant the sequence referred to as SEQ ID NO:2, and the complementary sequences and/or the sequences of polynucleotides that hybridize to the referred sequences in high stringent conditions
25 (hybridization in a mixture containing 5 x SSPE, 5x Denhart solution, 0.5% SDS (w/v) and 100 µg/ml salmon sperm DNA]. The membrane on which is hybridized the DNA, is washed 2 times during 10 minutes, in 2x SSPE, 0.1% SDS (w/v) at room temperature and then the membrane (or the filter) is immersed in a solution of 1 x SSPE, 0.1% SDS (w/v) during 15 minutes at 68°C and finally in a

solution of 1 x SSPE, 0.1% SDS (w/v) during 15 minutes at 68°C. The polynucleotides according to the invention are used for detecting *Enterococcus faecium* strains carrying a gene encoding resistance to streptogramin A.

5 By "active molecule" according to the invention is meant a molecule capable of inhibiting the activity of the purified polypeptide as defined in the present invention or capable of inhibiting the bacterial culture of *Enterococcus faecium* strains.

10 Thus, the polynucleotides of SEQ ID NO:2 and its fragment can be used to select nucleotide primers notably for an amplification reaction, such as the amplification reactions further described. PCR is described in the U.S. Patent No. 4,683,202 granted to Cetus Corp. The amplified fragments may identified by agarose or
15 polyacrylamide gel electrophoresis, or by a capillary electrophoresis, or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography, or ion exchange chromatography). The specificity of the amplification can be ensured by a molecular hybridization using as nucleic probes the polynucleotides derived from
20 SEQ ID NO:2 and its fragments, oligonucleotides that are complementary to these polynucleotides or fragments thereof, or their amplification products themselves.

25 Amplified nucleotide fragments are useful as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order detect the presence of a bacteria of *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A, in a biological sample. This invention also provides, the amplified nucleic acid

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fragments ("amplicons") defined herein above. These probes and amplicons can be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

5 Preferred nucleic acid fragments that can serve as primers according to the present invention are the following in the Fig. 1:

PRIMER F 5' -CAATATTGGAATTCGGGACTACACC-3' (SEQ ID NO:3)
EcoRI

10 nt 354 nt 378 gene vatD

PRIMER R 5' -CTGTTTATGAATTCAAGTGTGG-3' (SEQ ID NO:4)
EcoRI

nt 899 nt 878 gene vatD

The primers can also be used as oligonucleotide probes to specifically detect a polynucleotide according to the invention.

15 Other techniques related to nucleic acid amplification can also be used and are generally preferred to the PCR technique. The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at a recognition site (which is under a hemiphosphorothioate form), and on the property of a DNA polymerase to
20 initiate the synthesis of a new strand from the 3' OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously
25 synthesized strand being localized downstream.

The SDA amplification technique is more easily performed than PCR (a single thermostated water bath device is necessary and is faster than the other

amplification methods. Thus, the present invention also comprises using the nucleic acid fragment according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. The polynucleotides of SEQ ID NO:2 and its fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as:

- TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989;
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990;
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991; and
- TMA (Transcription Mediated Amplification).

The polynucleotides of SEQ ID NO:2 and its fragments, especially the primers according to the invention, are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as:

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991, who employ a thermostable ligase;
- RCR (Repair Chain Reaction), described by Segev et al. 1992;
- CPR (Cycling Probe Reaction), described by Duck et al. in 1990; and
- Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

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When the target polynucleotide to be detected is RNA, for example mRNA, a reverse transcriptase enzyme can be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA can be subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

Nucleic probes according to the present invention are specific to detect a polynucleotide of the invention. By "specific probes" according to the invention is meant any oligonucleotide that hybridizes with the polynucleotide of SEQ ID NO:2, and which does not hybridize with unrelated sequences. Preferred oligonucleotide probes according to the invention are SEQ ID NOS:5, 6, 7, or 8 or SEQ ID NOS:3 or 4.

In a specific embodiment, the purified polynucleotides according to the present invention encompass polynucleotides having at least 80% identity in their nucleic acid sequences with polynucleotide of SEQ ID NO:2. By percentage of nucleotide homology according to the present invention is intended a percentage of identity between the corresponding bases of two homologous polynucleotides, this percentage of identity being purely statistical and the differences between two homologous polynucleotides being located at random and on the whole length of said polynucleotides. The calculation was made according to the software GCG and the program "gap."

The oligonucleotide probes according to the present invention hybridize specifically with a DNA or RNA

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molecule comprising all or part of the polynucleotide of SEQ ID NO:2 under stringent conditions. As an illustrative embodiment, the stringent hybridization conditions used in order to specifically detect a polynucleotide according to the present invention are advantageously the following:

Prehybridization and hybridization are performed at 68°C a mixture containing:

- 5X SSPE (1X SSPE is .3 M NaCl, 30 mM tri-sodium citrate
- 5X Denhardt's solution
- 0.5% (w/v) sodium dodecyl sulfate (SDS); and
- 100 $\mu\text{g ml}^{-1}$ salmon sperm DNA

The washings are performed as follows:

- Two washings at laboratory temperature for 10 min. in the presence of 2 x SSPE and 0.1 % SDS;
- One washing at 68°C for 15 min. in the presence of 1 x SSPE, .1% SDS; and
- One washing at 68°C for 15 min. in the presence of 0.1 x SSPE and 0.1 % SDS.

The non-labeled polynucleotides or oligonucleotides of the invention can be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications. Examples of non-radioactive labeling of nucleic acid fragments are described in the French Patent No. FR 78 10975 or by Urdea et al. or Sanchez Pescador et al. 1988.

Other labeling techniques can also be used, such as those described in the French patents 2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al. 1988). A general method comprises immobilizing the nucleic acid that has been extracted from the biological sample on a substrate (nitrocellulose, nylon, polystyrene) and then incubating, in defined conditions, the target nucleic acid with the probe. Subsequent to the hybridization step, the excess amount of the specific probe is discarded, and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence, or enzyme activity measurement).

Advantageously, the probes according to the present invention can have structural characteristics such that they allow signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European Patent No. 0 225 807 (Chiron).

In another advantageous embodiment of the present invention, the probes described herein can be used as "capture probes", and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe, which recognizes a sequence of the target nucleic acid that is different from the sequence recognized by the capture probe.

The oligonucleotide fragments useful as probes or primers according to the present invention can be prepared by cleavage of the polynucleotide of SEQ ID NO:2

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by restriction enzymes, as described in Sambrook et al. in 1989. Another appropriate preparation process of the nucleic acids of the invention containing at most 200 nucleotides (or 200 bp if these molecules are double-stranded) comprises the following steps:

- synthesizing DNA using the automated method of beta-cyanethylphosphoramidite described in 1986;
- cloning the thus obtained nucleic acids in an appropriate vector; and
- purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

A chemical method for producing the nucleic acids according to the invention, which have a length of more than 200 nucleotides (or 200 bp if these molecules are double-stranded) comprises the following steps:

- Assembling the chemically synthesized oligonucleotides having different restriction sites at each end;
- cloning the thus obtained nucleic acids in an appropriate vector; and
- purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

The oligonucleotide probes according to the present invention can also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of or several bases, one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target

nucleic acid. Optionally, the substrate of the matrix can be a material able to act as an electron donor, the detection of the matrix positions in which hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a target nucleic acid are described in the European patent application No. 713 016, or PCT Application No. WO 95 33846, or also PCT Application No. WO 95 11995 (Affymax Technologies), PCT Application No. WO 97 02357 (Affymetrix Inc.), and also in U.S Patent No. 5,202,231 (Drmanac), said patents and patent applications being herein incorporated by reference.

The present invention also pertains to a family of recombinant plasmids containing at least a nucleic acid according to the invention. According to an advantageous embodiment, a recombinant plasmid comprises a polynucleotide of SEQ ID NO:2 or nucleic acid fragment thereof. More specifically, the following plasmid is part of the invention: pIP1801 or its fragments. Said fragments are derived from the use of restriction enzymes according to the restriction map of the gene *vatD*, as shown in Figure 3.

The present invention is also directed to the full length coding sequences of the *vatD* gene from *Enterococcus faecium* available using the purified polynucleotides according to the present invention, as well as to the polypeptide enzymes encoded by these full length coding sequences. In a specific embodiment of the present invention, the full length coding sequence of the *vatD* gene is isolated from a plasmid or cosmid library of

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the genome of *Enterococcus faecium* that has been screened with the oligonucleotide probe according to the present invention. The selected positive plasmid or cosmid clones hybridizing with the oligonucleotide probes of the invention are then sequenced in order to characterize the corresponding full length coding sequence, and the DNA insert of interest is then cloned in an expression vector conferring resistance to streptogramin A and related compounds.

A suitable vector for the expression in bacteria and in particular in *E. coli*, is the pQE-30 vector (QIAexpress) that allows the production of a recombinant protein containing a 6xHis affinity tag. The 6xHis tag is placed at the C-terminus of the recombinant polypeptide ATP binding motif conferring resistance to streptogramin A and related compounds.

The polypeptides according to the invention can also be prepared by conventional methods of chemical synthesis, either in a homogenous solution or in solid phase. As an illustrative embodiment of such chemical polypeptide synthesis techniques the homogenous solution technique described by Houbenweyl in 1974 may be cited.

The polypeptide conferring resistance to streptogramin A and related compounds is useful for the preparation of polyclonal or monoclonal antibodies that recognize the polypeptides or fragments thereof. The monoclonal antibodies can be prepared from hybridomas according to the technique described by Kohler and Milstein in 1975. The polyclonal antibodies can be prepared by immunization of a mammal, especially a mouse or a rabbit, with a polypeptide according to the

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invention that is combined with an adjuvant, and then by purifying specific antibodies contained in the serum of the immunized animal on a affinity chromatography column on which has previously been immobilized the polypeptide that has been used as the antigen.

Consequently, the invention is also directed to a method detecting specifically the presence of a polypeptide according to the invention in a biological sample. The method comprises:

- a) bringing into contact the biological sample with an antibody according to the invention; and
- b) detecting antigen-antibody complex formed.

Also part of the invention is a diagnostic kit for *in vitro* detecting the presence of a polypeptide according to the present invention in a biological sample. The kit comprises:

- a polyclonal or monoclonal antibody as described above, optionally labeled; and
- a reagent allowing the detection of the antigen-antibody complexes formed, wherein the reagent carries optionally a label, or being able to be recognized itself by a labeled reagent, more particularly in the case when the above-mentioned monoclonal or polyclonal antibody is not labeled by itself.

Indeed, the monoclonal or polyclonal antibodies according to the present invention are useful as detection means in order to identify or characterize a *Staphylococcal* strain carrying gene encoding resistance to streptogramin A.

The invention also pertains to:

- A purified polypeptide or a peptide fragment having at least 10 amino acids, which is recognized by antibodies directed against a polynucleotide sequence conferring resistance to streptogramin and related compounds, corresponding to a polynucleotide sequence according to the invention.

- A polynucleotide comprising the full length coding sequence of a *Enterococcus faecium* streptogramin A resistant gene containing a polynucleotide sequence according to the invention.

- A monoclonal or polyclonal antibody directed against a polypeptide or a peptide fragment encoded by the polynucleotide sequences according to the invention.

- A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the invention in a biological sample comprising:

- a) contacting bacterial DNA of the biological sample with a primer or a probe according to the invention, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;
- b) amplifying the nucleotide sequence using said primer or said probe; and
- c) detecting the hybridized complex formed between said primer or probe with the DNA.

A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

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a) a polynucleotide probe according to the invention; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

5 A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

10 a) a polynucleotide probe according to the invention; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

15 A method of screening active antibiotics for the treatment of the infections due to Gram-positive bacteria, comprising the steps of:

a) bringing into contact a Gram-positive bacteria having a resistance to streptogramin A and related compounds and containing the polynucleotide sequences according to the invention with the antibiotic; and

20 b) measuring an activity of the antibiotic on the bacteria having a resistance to streptogramins and related compounds.

25 A method of screening for active synthetic molecules capable of penetrating into a bacteria of the family of enterococcus, wherein the inhibiting activity of these molecules is tested on at least a polypeptide encoded by the polynucleotide sequences according to the invention comprising the steps of:

a) contacting a sample of said active molecules with the bacteria;

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b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.

An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by the polynucleotide sequences according to the invention, wherein the inhibiting activity of these molecules is tested on at least said polypeptide, said method comprising the steps of:

- a) extracting a purified polypeptide according to the invention;
- b) contacting the active molecules with said purified polypeptide;
- c) testing the capacity of the active molecules, at various concentrations, to inhibit the activity of the purified polypeptide; and
- d) choosing the active molecule that provides an inhibitory effect of at least 80 % on the activity of the said purified polypeptide.

In the inactivation by the O-acetylation of virginiamycin A mediated by *vatD*, the donor of acetyl group is probably acetyl coenzyme A. The acetylation reduced coenzyme A can react with 55'-dithio bis 2 nitrobenzoate (DTNB) to yield 5 thio 2 nitrobenzoate with a 1:1 stoichiometry. The 5 thio 2 nitrobenzoate is

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yellow and has a high extinction coefficient ($E = 00136 \text{ mM}^{-1} \text{ cm}^{-1}$) at $\lambda 412 \text{ nm}$. Therefore, the measurement of its appearance can be recorded by a spectrophotometer with great sensitivity.

5 As examples there are disclosed hereinafter the detection of chloramphenicol acetyl transferase activity. Similar conditions may be used for the detection of virginiamycin A activity to yield 5-thio-2-nitrobenzoate with a 1:1 stoichiometry. The thio-2-nitrobenzoate is
10 yellow and has a high extinction coefficient ($00136 \text{ mM}^{-1} \text{ cm}^{-1}$) at $\lambda 412 \text{ nm}$. Therefore, the measurement of its appearance can be recorded spectrophotometrically with great sensitivity.

Materials

- 15 - Bacterial strain(s) to be tested.
- Mueller-Hinton (MH) broth (Gram-negative bacteria) or brain heart infusion (BHI) broth (Gram-positive cocci)
- 50 ml centrifuge tubes
- 20 - Eppendorf tubes
- Low speed centrifuge
- Refrigerated bench centrifuge
- Sonicator
- Double beam recording spectrophotometer
25 equipped with a water jacketed cuvette
- Tris-Cl 1M (pH 6.0)
- Tris-Cl 1M (pH 7.8)
- Dithiothreitol (DTT) 0.01 M
- TDTT buffer: Tris-Cl 50 mM (pH 7.8)

DTT 20 μM

- Acetyl coenzyme A (CoASAc) 10 mM (PH 6.0) :
dissolve 8.2 mg of CoASAc in 1 ml of 5 mM Tris-Cl (pH 6.0). This solution can be stored frozen for 1 year in aliquots (100 μ l).
- 5, 5'-dithiobis-2-nitrobenzoic acid (DTNB) 10 mM (PH 7.8) : dissolve 20 μ g of DTNB in 0.5 ml of 1 M Tris-Cl (pH 7.8) and add 4.5 ml of distilled water. This solution should be make fresh each time.
- Reaction mixture: CoASAc (10 mM, pH 6.0):100 μ l
DTNB (10 mM, PH 7.8) :500 μ l
Tris-Cl (1 M, PH 7.8):920 μ l
H₂O up to 10 ml

This volume is sufficient for 15

reactions.

- Chloramphenicol (Cm) 10 mM (pH 7.8): dissolve 3.2 mg of Cm in 1 ml of 100 mM Tris-Cl (pH 7.8). heat 10 min in water bath at 100°C. Store at +4°C.

Protocol

Day 1

1. Inoculate separately 5 ml of MH broth with bacterial strains to be tested. Grow overnight at 37°C with moderate shaking.

Day 2

2. Inoculate separately 35 ml of MH broth with 1 ml of each overnight culture. Grow at 37°C with moderate shaking until the OD_{600nm} is 0.8.
3. Centrifuge the cells (8000 rpm, 10 min, 4°C). Discard the supernatant and wash the pellet in 1 ml of TDDT buffer. Centrifuge again and

resuspend the pellet in 1 ml of the same buffer.

4. Sonicate the cells at 4°C with 5 x 30 s pulses with 30 s rest in between.
5. Centrifuge the samples in an Eppendorf centrifuge (15000 rpm, 10 min, 4°C) to remove cell debris.
6. Transfer supernatants (S20) to other Eppendorf tubes and keep on ice until assayed. If the CAT assay is not performed on the same day, freeze the samples at -20°C. The CAT activity can be retained frozen for at least one month.
7. Pour 600 μ l of reaction mixture to reference cuvette and sample cuvettes equilibrated at 37°C in a double beam recording spectrophotometer. let stand 2 min ar adjust OD_{412nm} to 0.
8. Add 20 μ l of S20 to sample cuvettes, mix well, and record OD_{412nm} for 1-2 min to determine the background CAT activity.
9. When a constant slope is obtained, add 10 μ l of Cm to cuvettes, mix well and record the increase in absorbence (OD_{412nm}) for about 5 min. If the CAT activity is too high, a more reliable measure of activity can be obtained by diluting the S20.
10. Measure the amount of protein in the S20.
11. Determine the slope (OD_{412nm}/min) before and after adding Cm and then subtract the background slope from the sample slope. The CAT enzyme specific activity expressed in

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nmole/min/mg is $\Delta OD_{412nm}/0.0136/\text{mg protein}$
 [0.0136 being the extinction coefficient ($\text{mM}^{-1}\text{cm}^{-1}$ $\lambda 412\text{nm}$) of 5-thio-2-nitrobenzoate].

Notes

- 5 - Since the formation of 5-thio-2-nitrobenzoate is accompanied by the appearance of a yellow coloration, CAT activity can be qualitatively appreciated *de visu* in step 9.
- 10 - The crude extracts (S20) obtained from certain bacterial genera contain high thioesterase activity that may mask that of CAT since it also catalyzes the formation of reduced coenzyme A. On the
- 15 other hand, DTNB was reported to inhibit certain CTAs from Gram-negative bacteria. In both cases, partial purification of the enzyme or the use of an alternate
- 20 procedure is necessary to overcome these problems. Different methods for convenient CAT assays based on labelled acetyl
- coenzyme A (or butyryl coenzyme A) for acyl donor are available.
- 25 - Chloramphenicol analogs, such as 3'-desoxychloramphenicol, can be used to induce CAT expression in Gram-positive bacteria. This compound is not acetylated by CATs (free inducer) and has little effect on protein synthesis.
- Medium containing carbohydrates other than glucose may be used for the growth of

Gram-negative bacteria to avoid catabolic repression.

If an active molecule for inhibiting the activity of the bacterial enzyme (acetyl transferase) is added to a culture medium containing the resistant strain, the acetyl co-enzyme A present in said medium is not degraded. If the molecule to be tested is not active on the resistant bacteria, the amount of acetyl co-enzyme A decreases.

A test for screening the inhibiting activity of a molecule, for example, a new antibiotic or a new antibacterial agent, can comprise the following steps:

- a) adding purified active acetyl transferase vatD in a solution containing virginiamycin A at various concentrations, acetyl co-enzyme A,
- b) adding the molecule to be tested at various concentrations,
- c) revealing the presence of acetyl co-enzyme A activity and quantifying said acetyl coenzyme A, if necessary, and
- d) comparing the quantification of acetyl coenzyme A with a control without the new molecule.

A composition of a polynucleotide sequence encoding resistance to streptogramins and related compounds, or inducing resistance in Gram-positive bacteria, wherein said composition comprises a nucleotide sequence corresponding to the resistance phenotype of the plasmid pIP1807 deposited with the C.N.C.M. under the Accession No. I-2247 on July 7, 1999.

A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the

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invention in a biological sample, said method comprising the steps of:

- a) contacting said sample with an antibody according to the invention that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting said complex.

A diagnostic kit for *in vitro* detecting the presence of bacterium harboring the polynucleotide sequences according to invention in a biological sample, said kit comprising:

- a) a predetermined quantity of monoclonal or polyclonal antibodies according to the invention;
- b) reagents necessary to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide sequences; and
- c) reagents necessary for detecting said complex between the antibodies and the polypeptide encoded by said polynucleotide sequences.

Plasmids containing the polynucleotides from *Enterococcus faecium*, which confer streptogramin A resistance have been inserted into vectors, which have been deposited at the Collection Nationale de Cultures de Microorganismes ("C.N.C.M.") Institut Pasteur, 28, rue du Docteur Roux, 75724 Paris Cedex 15 France on July 7, 1999, as follows:

Plasmid
pIP1801

Accession No.
I-2247

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This invention will now be described in greater detail in the following Example.

Example

A collection of 51 *E. faecium* strains was studied for resistance to streptogramins. The strains were isolated from fecal samples from poultry (n = 22), pigs (n = 5), farmers (n = 19) and (sub)urban residents (n = 5) in the Netherlands (Table 1). *sata* was previously found in 19 strains and *vgb* in a single strain by PCR (14). The *E. faecium* strains were analyzed for nucleotide sequences hybridizing at high stringency (65°C) with the eight genes previously found in staphylococcal and enterococcal plasmids conferring resistance to the mixtures: *sata* (18), *vat* (9), *vatB* (3), *vatC* (6), *vga* (7) and *vgaB* (4) conferring resistance to A compounds and the two genes, *vgb* (8) and *vgbB* (6), encoding lactonases hydrolyzing B compounds. Nineteen of the strains carried *sata* and the combination of *vat* and *vgb* was detected in a single strain, KH6 (Table 1). These two latter genes are contiguous and in the same relative position as in the staphylococcal plasmids in which *vat-vgb* are carried by a DNA fragment originating from the *E. faecalis* plasmid, pAM β 1 (5).

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Table 1. Relevant characteristics of the 51 *E. faecium* strains isolated in the Netherlands.

Strain		<i>Sg^R</i> genes	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing <i>Hind</i> III fragment (2)
4	pig (Weert)	vatD	1.8
14	pig (Weert)	vatD	1.8
17	pig (Weert)	satA	4.5*
18	pig (Weert)	satA	3.8*
19	pig (Weert)	satA	3.8*
K12	turkey	vatD	6.0*
K13	turkey	vatD	5.6*
K14	turkey	vatD	6.0*
K15	turkey	vatD	5.6*
K36	turkey	satA	6.0*
K40	turkey	vatD	3.6*
KS30	turkey	vatD	1.4
KS31	turkey	vatD	1.4
KS33	turkey	vatD	1.4
SK1	broiler	vatD	3.2*
SK2	broiler	vatD	3.2*
SK3	broiler	vatD	> 10*
SK6	broiler	satA	7.0*
SK7	broiler	vatD	5.6*
SK8	broiler	vatD	5.6*
SK13	broiler	vatD	3.2*

PATENT
Attorney Docket No. 03495-0193

<i>Strain</i>		<i>Sg^R genes</i>	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing <i>Hind</i> III fragment (2)
SK19	broiler	vatD	3.9*
PS17	broiler	vatD	4.3*
PS22	broiler	satA	4.0*
PS26	broiler	vatD	4.3*
PS35	broiler	vatD	4.3*
PS42	broiler	vatD	4.3*
KH2	turkey farmer	vatD	5.6*
KH4	turkey farmer	satA	3.9*
KH5	turkey farmer	vatD	7.3*
KH6	turkey farmer	vatD vat-vgb	5.6* 8.9
KH7	turkey farmer	vatD	2.5
KH15	turkey farmer	satA	2.3*
KH18	turkey farmer	vatD	2.3
KH19	turkey farmer	vatD	2.3
KH29	turkey farmer	vatD	2.3*
KH36	turkey farmer	satA	3.9
KH39	turkey farmer	vatD	2.9
LKH2	chicken farmer	satA	4.0*
LKH4	chicken farmer	satA	4.3*
SKH4	chicken farmer	vatD	2.5*
SKH8	chicken farmer	satA	5.6*
SKH11	chicken farmer	vatD	2.5

Strain		Sg ^R genes	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing <i>Hind</i> III fragment (2)
SKH16	chicken farmer	satA	4.5*
SKH18	chicken farmer	satA	3.9*
SKH23	chicken farmer	satA	3.9*
M2	Suburban (Weert)	satA	3.9*
M5	suburban (Weert)	vatD	1.9
R2	suburban (Roermond)	satA	3.9*
R24	suburban (Roermond)	satA	3.9*
W3	suburban (Weert)	satA	4.0*

(1) The strains were screened for Sg^R genes by hybridization at high annealing temperature (65°C) (2) with probe consisting of (i) recombinant plasmids containing DNA inserts from within each of the following genes: *vat*(9), *vatB* (3), *vatC* (6), *vga* (7) or *vgaB* (4) or (ii) DNA fragments amplified from *satA* (18) or *vatD* (this study) by PCR with the following pairs of primers: *sat1* (nt position: 189-210 in *satA*, Acc. No. L12033) and *sat2* (nt position: 760-782 in *sat_* or *vatD*-F (nt position: 354-378 in *vatD*, Acc. No. AF153312) and *vatD*-R (nt position: 878-899 in *vatD*).

(2) The *Hind*III fragments indicated with an asterisk were detected in extrachromosomal DNA bands (≥ 40 kb)

migrating above the chromosomal DNA fragments of the uncleaved total cellular DNA, in agarose gel electrophoresis in Tr- acetate buffer. In the other strains, the hybridizing bands comigrated with the chromosomal fragments, but the hybridization signals were as strong as those of the extrachromosomal DNA, suggesting that they may be carried plasmids.

Thirty-one of the tested *E. faecium* strains did not contain any of the eight genes investigated. PCR experiments were carried out at low annealing temperature (40°C) with a pair of degenerate primers, M and N (3, 16), designed to amplify a DNA fragment from any sequence encoding a streptogramin A acetyltransferase containing two well conserved motifs, III and IV (3, 6, 16). A DNA fragment of the expected size (147 nt) was amplified from the cellular DNA of all the strains. The amplicon obtained with the strain K14 was sequenced using oligonucleotides M and N as primers. Its sequence was only 60.4 % to 68.6% similar to the SgA acetyltransferase genes (*vat*, *vatB*, *vatC*, *sata*), suggesting that the amplicon was from a different gene. A 5 kb *HindIII* fragment hybridizing with the sequenced amplicon was isolated from the cellular DNA of strain K14 and inserted into the *HindIII* site of pUC18. The resulting plasmid, pIP1798, was used to sequence 1080 nt of the insert including the sequences hybridizing with the 147 bp amplicon.

The sequence (registered in the GenBank EMBLdata Library under Accession No. AF153312) contains a 642 bp gene including an ATG start codon preceded, 6 nt upstream, by a putative ribosome-binding site. The free

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energy of association of the most stable structure between this site and the 3' terminus of the 16S rRNA was -61.5 kJ/mol. This gene, named *vatD*, is similar to those encoding SgA acetyltransferases, *sataA*, *vat*, *vatB*, and *vatC* (54.3, 58.0, 60.0, and 60.1 % similarity, respectively). *vatD* encodes a putative 214 aa protein of 23,775 Da similar to xenobiotic acetyltransferases (17). It is most similar to the SgA acetyltransferases, *SatA*, *Vat*, *VatB*, and *VatC* (48.5, 50.0, 59.9 and 50.9 % identical amino acids, respectively).

Most *vat*-related genes in staphylococcal plasmids are contiguous to and downstream from another streptogramin-resistance (*Sg^R*) gene. The pairs of genes are probably co-transcribed (12). However, analysis of the 270 and 170 nt sequences flanking *vatD* did not suggest the presence of any contiguous *Sg^R* gene.

A DNA fragment of 858 nt containing *vatD* (nt 104 to nt 961, Accession No. AF153312) was amplified from pIP1798 and inserted between the *EcoRI* and *SmaI* sites of the shuttle vector, pOX7 (11). The resulting plasmid, pIP1801, introduced by electroporation in the *S. aureus* recipient, RN4220 (15), conferred resistance to pristinamycin IIA (MICs: 2 µg/ml for RN4220 [pOX7] and 8 µg/ml for RN4220 [pIP1801]).

The presence of *vatD* in other strains was tested by hybridization experiments at high stringency. Nucleotide sequences hybridizing with *vatD*-probe were detected in the 32 strains which did not carry *sataA*, including the strain containing *vat-vgb* (Table 1). Total cellular DNA of strain KH6 was subjected to agarose gel electrophoresis. The *vatD* and *vat-vgb* sequences migrated

to different positions, suggesting that they are not carried by the same plasmid.

The distribution of the streptogramin-resistance genes in the collection of *E. faecium* studied was clearly different from that found in staphylococci (2). It is worth checking whether the high prevalence of *vatD* in this collection, is also observed among infectious clinical isolates.

* * *

In summary, the present invention pertains to polynucleotides derived from *Enterococcus faecium* genes encoding resistance to streptogramin A and chemically related compounds. This invention also relates to the use of the polynucleotides as oligonucleotide primers or probes for detecting *Enterococcus faecium* strains that are resistant to streptogramin A and related compounds in a biological sample.

In another embodiment, the present invention is directed to the full length coding sequences of the *Enterococcus faecium* genes encoding for resistance to streptogramin A and to the polypeptides expressed by these full length coding sequences.

Further, this invention relates to the use of the expressed polypeptides to produce specific monoclonal or polyclonal antibodies that serve as detection means in order to characterize any *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A and chemically related compounds.

The present invention is also directed to diagnostic methods for detecting specific strains of *Enterococcus faecium* expected to be contained in a biological sample.

The diagnostic methods use the oligonucleotide probes and primers as well as the antibodies of the invention raised against VatD protein or its fragments.

5 The invention relates also to a method of screening of molecules, which are capable to inactivate the acetyl transferase activity in bacteria. A bacterial culture, which is resistant to virginiamycin A, can grow in the presence of virginiamycin, but cannot grow if a new molecule active against acetyl transferase activity is
10 added to the culture medium.

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The following publications are cited herein. The entire disclosure of each publication is relied upon and incorporated by reference herein.

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SEQUENCE IDENTIFIERS

SEQ ID NO:1

1 MTIPDANAIY HNSAIKEVVF IKNVIKSPNI EIGDYTYDD PVNPTDFEKH
 51 VTHHYEFLGD KLIIGKFCSL ASGIEFIMNG ANHVMKGIST YPFNILGGDW
 5 101 QQYTPELTDL PLKGD TVVGN DVWFGQNVTV LPGVKIGDGA IIGANSVVTK
 151 DVAPYTIVGG NPIQLIGPRF EPEVIQALEN LAWWNKDIEW ITANVPKLMQ
 201 TTPTLELINS LME

SEQ ID NO:2

10 ATGACTATAC CTGACGCAAA TGCAATCTAT CATAACTCAG CCATCAAAGA GGTTGTCTTT
 ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC
 CCAGTAAATC CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC
 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT CATGAACGGT
 GCCAACCACG TAATGAAAGG TATTTCTGACT TATCCATTTA ATATATTAGG TGGCGATTGG
 15 CAACAATACA CTCCTGAACT GACTGATTTG CCGTTGAAAG GTGATACTGT AGTCGGAAAT
 GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC
 ATTATCGGAG CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGCC
 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGGAAG TTATTCAAGC ATTAGAAAAT
 CTGGCATGGT GGAATAAAGA TATTGAATGG ATAAGTCTA ATGTTCTTAA ACTAATGCAA
 ACAACACCCA CACTTGAATT GATAAACAGT TTAATGGAAA AA

20 5'- CAATATTGGAATTCGGGACTACACC - 3' primer F SEQ ID NO:3
 EcoRI

5'- CTGTTTATGAATTCAGTGTGG - 3' primer R SEQ ID NO:4
 EcoRI

Seq. 4
 25 I M N G A N H SEQ ID NO:5

5'- ATH ATG AAY GCN AAY CAY - 3' primer M SEQ ID NO:6

G N D V W SEQ ID NO:7

5'- CCA NAC RTC RTT NCC - 3' primer N SEQ ID NO:8

(abbreviations: H=A,T,C Y=C,T N=A,C,T,G R=A,G)

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PATENT
Attorney Docket No. 03495-0193

A N A I Y H N S SEQ ID NO:9

5'- GCA AAT GCA ATC TAT CAT AAC TCA - 3' SEQ ID NO:10

M Q T T P T L E L SEQ ID NO:11

5'- ATG CAA ACA ACA CCC ACA CTT GAA TTG - 3' SEQ ID NO:12

5 5'- TAGAAAGAATTCAGTGATTGTGG - 3' primer A SEQ ID NO:13
EcoRI

5'- GGATTCACTAAATAGTAAAGGCCGTG - 3' primer B SEQ ID NO:14
HaeIII

SEQ ID NO:15

10 AAATTTAGG CGCACAAAAA GAAAGAGTGT GACAAAACAT GGTTATGCTA CATGTTTAAAG
GTAAAAATAG TTATGTCACA ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAATTAA
AATTAAATAA CTCAATTCGG AGGTACTAAC CTGACTATAC CTGACGCAA TGCAATCTAT
CATAACTCAG CCATCAAAGA GGTGACTTT ATCAAGAACG TGATCAAAG TCCCAATATT
15 GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTT TGAGAAACAC
GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT TTGTTCTCTC
GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG TAATGAAAGG TATTTGACT
TATCCATTTA ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAACT GACTGATTTG
CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC
CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA
20 GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG ACCAAGATTT
GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG
ATAACTGCTA ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT
TTAATGGAAA AATAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT TGTTTACACG
G

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WHAT IS CLAIMED IS:

1. A purified nucleic acid molecule comprising the DNA sequence of SEQ ID NO:2.

2. A purified nucleic acid molecule encoding an amino acid sequence comprising the sequence of SEQ ID NO:1.

3. A purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of any one of claims 1 or 2 under conditions of moderate stringency.

4. The purified nucleic acid molecule as claimed in claim 3, wherein said isolated nucleic acid molecule is derived by *in vitro* mutagenesis from SEQ ID NO:2 to NO 15.

5. A purified nucleic acid molecule degenerate from SEQ ID NOS:5, 6, 7, or 8 as a result of the genetic code.

6. A purified nucleic acid molecule, which encodes vatD polypeptide, an allelic variant of vatD polypeptide DNA, or a homolog of vatD polypeptide DNA.

7. A recombinant vector that directs the expression of a nucleic acid molecule selected from the group consisting of the purified nucleic acid molecules of claims 1, 2, 5, and 6.

8. A recombinant vector that directs the expression of a nucleic acid molecule of claim 3.

9. A recombinant vector that directs the expression of a nucleic acid molecule of claim 4.

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10. A purified polypeptide encoded by a nucleic acid molecule selected from the group consisting of the purified nucleic acid molecules of claims 1, 2, 5, and 6.

11. A purified polypeptide according to claim 10 having a molecular weight of approximately 23,775 kDa as determined by SDS-PAGE.

12. A purified polypeptide according to claim 10 in non-glycosylated form.

13. A purified polypeptide encoded by a nucleic acid molecule of claim 3.

14. A purified polypeptide according to claim 13 in non-glycosylated form.

15. A purified polypeptide encoded by a nucleic acid molecule of claim 4.

16. A purified polypeptide according to claim 15 in non-glycosylated form.

17. Purified antibodies that bind to a polypeptide of claim 10.

18. Purified antibodies according to claim 17, wherein the antibodies are monoclonal antibodies.

19. Purified antibodies that bind to a polypeptide of claim 13.

20. Purified antibodies according to claim 19, wherein the antibodies are monoclonal antibodies.

21. Purified antibodies that bind to a polypeptide of claim 15.

22. Purified antibodies according to claim 21, wherein the antibodies are monoclonal antibodies.

23. A host cell transfected or transduced with the vector of claim 7.

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24. A method for the production of vatD polypeptide comprising culturing a host cell of claim 23 under conditions promoting expression, and recovering the polypeptide from the culture medium.

5 25. The method of claim 24, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

26. A host cell transfected or transduced with the vector of claim 8.

10 27. A method for the production of vatD polypeptide comprising culturing a host cell of claim 26 under conditions promoting expression, and recovering the polypeptide from the culture medium.

15 28. The method of claim 27, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

29. A host cell transfected or transduced with the vector of claim 9.

20 30. A method for the production of vatD polypeptide comprising culturing a host cell of claim 29 under conditions promoting expression, and recovering the polypeptide from the culture medium.

25 31. The method of claim 30, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

32. The plasmid deposited at CNCM under the Accession Number I-2247.

33. An immunological complex comprising a vatD polypeptide and an antibody that specifically recognizes said polypeptide.

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34. A method of detecting a bacterium in a biological sample that harbors a polynucleotide sequence according to claim 1, said method comprising the steps of:

- a) contacting bacterial DNA of the biological sample with a primer or a probe according to claim 1 or 3 to 6, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;
- b) amplifying the nucleotide sequence using said primer or said probe; and
- c) detecting a hybridized complex formed between said primer or probe and the DNA.

35. A kit for detecting a bacterium that is resistant to a streptogramin and harbors a polynucleotide sequence according to claim 1, said kit comprising:

- a) a polynucleotide probe according to claim 19 or 20; and
- b) reagents to perform a nucleic acid hybridization reaction.

36. A kit for detecting a bacterium that is resistant to a streptogramin and harbors a polynucleotide sequence according to claim 2, said kit comprising:

- a) a polynucleotide probe according to claim 19 or 20; and
- b) reagents to perform a nucleic acid hybridization reaction.

37. A method of screening an active antibiotic for treating a Gram-positive bacterial infection, comprising the steps of:

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- a) contacting the antibiotic with Gram-positive bacteria that are resistant to a streptogramin and contain a polynucleotide sequence according to claim 1; and
- 5 b) determining the activity of the antibiotic on the bacteria.

38. A method of screening for active synthetic molecules capable of penetrating into a bacteria of the enterococcus family, wherein an inhibiting activity of the molecules is tested on at least a polypeptide encoded by a polynucleotide sequence according to claim 1, the method comprising the steps of:

10

- a) contacting a sample of said active molecules with the bacteria;
- 15 b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
- c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.
- 20

39. An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by a polynucleotide sequence according to claim 1, said method comprising the steps of:

25

- a) contacting the active molecules with said polypeptide;
- b) testing the capacity of the active molecules, at various concentrations, to inhibit the activity of the polypeptide; and

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- c) choosing the active molecule that provides an inhibitory effect of at least 80 % on the activity of the said polypeptide.

40. A method of detecting a bacterium in a biological sample that harbors a polynucleotide sequence according to claim 2, said method comprising the steps of:

- a) contacting said sample with an antibody according to claim 17 that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting a complex formed between the antibody and the polypeptide.

41. A diagnostic kit for *in vitro* detection of a bacterium harboring the polynucleotide sequences according to claim 2, said kit comprising:

- a) a predetermined quantity of monoclonal or polyclonal antibodies according to claim 17;
- b) reagents to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide sequences; and
- c) reagents for detecting a complex formed between the antibodies and the polypeptide encoded by said polynucleotide sequences.

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Attorney Docket No. 03495-0193

A gene encoding an acetyltransferase inactivating streptogramin A was isolated from an *Enterococcus faecium* strain and sequenced. The gene, designated vatD, encodes a 23,775 kDa protein exhibiting 48.5 to 59.9 % amino acid identity with four other enzymes with the same activity, Vat, VatB, VatC and SatA.

5

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1 CCCTTTAAAG AGGGCTTTTA TATATTAATC ACAAATCACT TATCACAAAT
 51 CACAAGTGAT TTGTGATTGT TGATGATAAA ATAAGAATAA GAAGAAATAG
 101 AAAGAAGTGA GTGATTGTGG GAAATTTAGG CGCACAAAAA GAAAGAGTGT
 151 GACAAAACAT GGTTATGCTA CATGTTTAAG GTAAAAATAG TTATGTCACA
 201 ACTACTTATT TTTTACCCTA ATCTTCTAGA CTATAATTAA AATTAAATAA
 XbaI
 M T I P D A N A I Y
 251 CTCAATTCGG AGGTACTAAC ATGACTATAC CTGACGCAA TGCAATCTAT
 RBS START
 H N S A I K E V V F I K N V I K S
 301 CATAACTCAG CCATCAAAGA GGTGTCTTT ATCAAGAACG TGATCAAAAG
 DdeI DpnI
 P N I E I G D Y T Y Y D D P V N
 351 TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC
 SspI
 P T D F E K H V T H H Y E F L G D
 401 CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC
 K L I I G K F C S L A S G I E F I
 451 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT
 M N G A N H V M K G I S T Y P F
 501 CATGAACGGT GCCAACCACG TAATGAAAGG TATTTCGACT TATCCATTTA
 TaqI
 N I L G G D W Q Q Y T P E L T D L
 551 ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAAC TACTGATTGG
 P L K G T V V G N D V W F G Q N V
 601 CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA
 T V L P G V K I G D G A I I G A
 651 TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG
 N S V V T K D V A P Y T I V G G N
 701 CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGGC
 P I Q L I G P R F E P E V I Q A L
 751 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGGAAG TTATTTCAAGC
 XmnI
 E N L A W W N K D I E W I T A N
 801 ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG ATAAGTCTA
 N V P K L M Q T T P T L E L I N S
 851 ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT
 L M E K *
 STOP
 901 TTAATGGAAA AATAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT
 951 TGTTTACACG GCCTTTACTA TTAGTGAAT CCAATTTATT AATAATAGAT
 HaeIII
 1001 ATGATATACC AGTAAAAAAT AACTAGCCA CCTCTGGCGG TACTCTACTC
 1051 GTATATTTTA TTACGACCT TCTGATGATA

FIGURE 1

1080 bp : restriction map

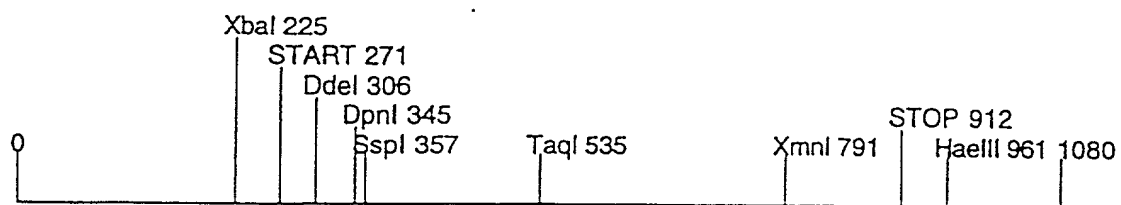


FIGURE3